TEAM 6

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/487,032*

DATE: 02/23/96
TIME: 11:34:47

INPUT SET: S8924.raw

> This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5        (i) APPLICANT: DOUGLAS SMITH
 6
 7       (ii) TITLE OF INVENTION:NUCLEIC ACID AND AMINO ACID SEQUENCES
 8            RELATING TO HELICOBACTER PYLORI FOR
 9            DIAGNOSTICS AND THERAPEUTICS
10
11      (iii) NUMBER OF SEQUENCES:  880
12
13      (iv) CORRESPONDENCE ADDRESS:
14            (A)  ADDRESSEE: LAHIVE & COCKFIELD
15            (B)  STREET: 60 State Street, Suite 510
16            (C)  CITY: Boston
17            (D)  STATE: Massachusetts
18            (E)  COUNTRY: USA
19            (F)  ZIP: 02109-1875
20
21       (v) COMPUTER READABLE FORM:
22            (A)  MEDIUM TYPE: Floppy disk
23            (B)  COMPUTER: IBM PC compatible
24            (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
25            (D)  SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27      (vi) CURRENT APPLICATION DATA:
28            (A)  APPLICATION NUMBER: US 08/487,032
29            (B)  FILING DATE: 07-JUNE-1995
30
31    (viii) ATTORNEY/AGENT INFORMATION:
32            (A)  NAME: Mandragouras, Amy E.
33            (B)  REGISTRATION NUMBER: 36,207
34            (C)  REFERENCE/DOCKET NUMBER: GTN-001
35
36      (ix) TELECOMMUNICATION INFORMATION:
37            (A)  TELEPHONE: (617)227-7400
38            (B)  TELEFAX: (617)227-5941
39
```

See notes throughout →

ERRORED SEQUENCES FOLLOW:

INPUT SET: S8924.raw

```
5923    (2) INFORMATION FOR SEQ ID NO:149:
5924
5925         (i) SEQUENCE CHARACTERISTICS:
5926             (A) LENGTH: 1017 base pairs
5927             (B) TYPE: nucleic acid
5928             (C) STRANDEDNESS: double
5929             (D) TOPOLOGY: circular
5930
5931        (ii) MOLECULE TYPE: DNA (genomic)
5932
5933       (iii) HYPOTHETICAL: NO
5934
5935        (iv) ANTI-SENSE: NO
5936
5937        (vi) ORIGINAL SOURCE:
5938             (A) ORGANISM: Helicobacter pylori
5939
5940
5941
5942        (xi) SEQUENCE DESCRIPTION: PHOSPHOMANNO:UTASE:
5943
5944   ATGATCACTG GCTCTCACAA CCCCAAAGAA TACAACGGCT TTAAAATCAC GCTCAATCAA      60
5945
5946   AACCCGTTTT ATGGCAAGGA CATTCAGGCT TTAAAAAACA CGCTTTTAAA CGCAAAGCAT     120
5947
5948   GAAATAAAGC CCCTAAAAGA AACGCCAGAG AAAGTCAATG CCCTAGAAGC GTATCATCGC     180
5949
5950   TATTTGATCA AGGATTTTAA GCATTTAAAA AATCTTAAAT ACAAAATCGC CCTGGATTTT     240
5951
5952   GGTAATGGCG TGGGGGCGTT AGGATTAGAG CCGATTTTAA AGGCTTTAAA CATTGATTTT     300
5953
5954   AGCAGCCTTT ATAGCGATCC TGATGGGGAT TTTCCTAACC ACCACCCAGA CCCTAGCGAA     360
5955
5956   GCGAAAAACT TAAAAGACTT AGAAAAACAC ATGCGAGAAA ACGCTATTTT AATAGGCTTT     420
5957
5958   GCTTTTGATG GCGATGCGGA TAGGATTGCG ATGCTAAGCT CTCATCATAT CTATGCGGGC     480
5959
5960   GATGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC AAGGCATCAC CCCTTTTGTG     540
5961
5962   ATCGGCGAAG TCAAATGCTC TCAAGTGATG TATAACGCAA TCAATACTTT TGGTAAGACG     600
5963
5964   CTCATGTATA AAACCGGGCA TAGCAATTTA AAAATCAAGC TCAAAGAAAC TAATGCGCAT     660
5965
5966   TTTGCGGCTG AAATGAGCGG GCATATCTTT TTTAAAGAAC GCTATTTTGG CTATGATGAC     720
5967
5968   GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG AACAAAGTCC AAGCGACTTG     780
5969
5970   GAAAACACCA TTAAAAACCT CCCCTATTCC TACACCACGC CTGAAGAAAA AATCGCCGTG     840
5971
5972   AGCGAAGAAG AAAAATTTGA AATCATTCGC AACTTACAAG AAGCGCTTAA AAACCCGCCA     900
5973
5974   AGCCATTTCC CTACAATCAA AGAAATCATC AGCATTGATG GCGTGAGAGT GGTTTTTGAA     960
5975
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INPUT SET: S8924.raw

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5976    CATGGCTTTG GGCTTATTCG CGCAAGCAAC ACCCACCCCC TATTTAGTCA GCCGCTT        1017
5977
5978
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7253    (2) INFORMATION FOR SEQ ID NO:179:
7254
7255        (i) SEQUENCE CHARACTERISTICS:
-->  7256.         (A) LENGTH: 264 base pairs
7257               (B) TYPE: nucleic acid
7258               (C) STRANDEDNESS: double
7259               (D) TOPOLOGY: circular
7260
7261        (ii) MOLECULE TYPE: DNA (genomic)
7262
7263    (iii) HYPOTHETICAL: NO
7264
7265    (iv) ANTI-SENSE: NO
7266
7267    (vi) ORIGINAL SOURCE:
7268          (A) ORGANISM: Helicobacter pylori
7269
7270    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:
7271
7272    GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA        60
7273
7274    GGGGTGTTGT TAGCATGTTT TTATCTTTTA GACGCTTATT ATCTCATGCA AGAAAGGCTG       120
7275
7276    TTTAGGGAGC AATACCAATG GCTAATAAAA AACCGACTTA AAACCGATGA AAGGCTGTTT       180
7277
7278    GAAGTCTTCC CTATTCATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCGTTCGT       240
7279
7280    TTAGTCTTTT CCCCTATTGG GCGT                              $%(, ,   La j (   Ia
7281        H     A     P      T     ( D  !  E $ J AqI1     b   dvQL _  FH iq acid
-->  7282         (C) STRANDEDNESS: double
-->  7283         (D) TOPOLOGY: circular
7284
7285    (ii) MOLECULE TYPE: DNA (genomic)
7286
7287    (iii) HYPOTHETICAL: NO
7288
7289    (iv) ANTI-SENSE: NO
7290
-->  7291    (vi) O NâOTAAAGCGGTC       240
7292
7293    TTTTTCACCC ACCATACTTT AAAGGCTTCG TTTGAGCCGA CTAACCACAT CAATTATAGA       300
7294
7295    GGGCATGACT ATGTGTTGGA TAATGTGCAT TTCCACGCCC CTATGGAGTT TTTAATCAAT       360
7296
7297    AATAAAACCA GGCCTTTGAG CGCGCATTTC GTGCATAAAG ACGCTAAAGG GCGTTTGTTG       420
7298
7299    GTGTTAGCGA TTGGTTTTGA AGAAGGGAAA GAAAACCCCA ACCTTGATCC TATTTTAGAA       480
7300
7301    GGCATTCAAA AGAAACAAAA TCTTAAAGAG GTGGCTTTAG ACGCTTTCTT GCCTAAAAGC       540
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[handwritten note:] PTO had problems reading your diskette. Here is some evidence that there may have been some bad sectors on the disk

INPUT SET: S8924.raw

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7304
7305    TGGTTTGTCA TAGAAGAACC TTTGGAAGTT TCTGCCAAAC AATTGGCTGA AATCAAAAAA        660
7306
7307    CGCATGAAAA ATTCGCCCAA CCAACGCCCC GTCCAGCCTG ACTACAACAC CGTGATCATT        720
7308
7309    AAAAGCTCGG CTGAGACCCG C                                                  741
7310
7311
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```
-->  7312    (2) INFORMATION FOR SEQ ID NO:131:        JUMps back to 131
     7313
     7314            (i) SEQUENCE CHARACTERISTICS:
     7315                    (A) LENGTH: 1266 base pairs
     7316                    (B) TYPE: nucleic acid
     7317                    (C) STRANDEDNESS: double
     7318                    (D) TOPOLOGY: circular
     7319
     7320        (ii) MOLECULE TYPE: DNA (genomic)
     7321
     7322      (iii) HYPOTHETICAL: NO
     7323
     7324       (iv) ANTI-SENSE: NO
     7325
     7326       (vi) ORIGINAL SOURCE:
     7327                    (A) ORGANISM: Helicobacter pylori
     7328
     7329       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:
     7330
     7331    ATGAAAATTT CTTTATTGGG GCATGGAAAA ACCACTCTAG CCCTAGGGCG TTTTTTTAAA        60
     7332
     7333    AAAAACCATA ATGAAGTCAA ATTTTTTGAT GATAAATTCC CTGCATTTTT TAAGGATAGC       120
     7334
     7335    GAGGGTTTTC TTTGCTACCC TAGTAAGGAT TTTAACCCTA ATGATTCCCA ACTAGAAATC       180
     7336
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     7338
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     7342
     7343    AAGGCTGTGA GTGGGGGGAA TATCGGCACG CCCTTGATTG AATTGTTTGA AAAACGATCG       420
     7344
     7345    CCCTTGTGGG TGCTAGAAAC AAGCTCCTTT TCTTTGCATT ACACTAATAA GGCTTACCCT       480
     7346
     7347    TTAATCTACT TGCTCATCAA TGTGGAAGCC GATCATTTGA CTTGGCATTG CAATTTTGAA       540
     7348
     7349    AATTATTTGA ACGCTAAACT CAAGGTTTTA ACATTGATGC CTAAAACTTC GCTCGCTATC       600
     7350
     7351    CTCCCTTTAA AATTCAAAGA ACACCCTATT GTTCAAAACT CGCAAGCGCA AAAAATCTTT       660
     7352
     7353    TTTGACAAAA GCGAAGAGGT TTTAGAGTGT TTAAAAATCC CTTCTAACGC CCTTTTTTTT       720
```

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INPUT SET: S8924.raw

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7354
7355   AAGGGAGCGT TTTTATTAGA CGCGGCTTTA GCCCTTTTAG TTTATGAGCA ATTTTTAAAA      780
7356
7357   ATAAAGAATT TAAAATGGCA AGATTATAGA GAAAACGCCC TTAAAAGACT GAACGCTTTT      840
7358
7359   AAAATCGGCT CGCATAAAAT GGAAGAATTT AGGGATAAAC AAGGGCGTTT GTGGGTAGAT      900
7360
7361   GACAGCAAAG CCACGAATAT TGATGCCACC TTACAAGCCC TAAAAACCTT TAAAAACCAA      960
7362
7363   AAAATCCATT TGATTTTAGG GGGCGATATT AAAGGGGTCA ATTTAACCCC CCTTTTTGAA     1020
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7365   GAGTTTAAAA ACTATAAAAT AAGCCTTTAT GCCATAGGAT CAAGCGCTTC TATCATACAA     1080
7366
7367   GCCTTAGCGT TAGAATTTAA TGTTTCTTGT CAGGTTTGTT TGAAGTTAGA AAAAGCGGTT     1140
7368
7369   CAAGAAATTA AAAGCGTTTT ATTACAAAAT GAAGTCGCTT TGCTTTCACC TAGCGCGGCC     1200
7370
7371   AGTTTGGATC AATTTTCTTC GTATAAAGAA AGGGGTGAAA AATTCAAAGC GTTTGTTTTA     1260
7372
7373   AAAGAT                                                               1266
7374
7375
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8045   (2) INFORMATION FOR SEQ ID NO:149:
8046
8047          (i) SEQUENCE CHARACTERISTICS:
8048               (A) LENGTH: 1017 base pairs
8049               (B) TYPE: nucleic acid
8050               (C) STRANDEDNESS: double
8051               (D) TOPOLOGY: circular
8052
8053          (ii) MOLECULE TYPE: DNA (genomic)
8054
8055         (iii) HYPOTHETICAL: NO
8056
8057          (iv) ANTI-SENSE: NO
8058
8059          (vi) ORIGINAL SOURCE:
8060               (A) ORGANISM: Helicobacter pylori
8061
8062
8063
-->  8064          (xi) SEQUENCE DESCRIPTION: PHOSPHOMANNOMUTASE:
8065
8066   ATGATCACTG GCTCTCACAA CCCCAAAGAA TACAACGGCT TTAAAATCAC GCTCAATCAA       60
8067
8068   AACCCGTTTT ATGGCAAGGA CATTCAGGCT TTAAAAAACA CGCTTTTAAA CGCAAAGCAT      120
8069
8070   GAAATAAAGC CCCTAAAAGA AACGCCAGAG AAAGTCAATG CCCTAGAAGC GTATCATCGC      180
8071
8072   TATTTGATCA AGGATTTTAA GCATTTAAAA AATCTTAAAT ACAAAATCGC CCTGGATTTT      240
8073
8074   GGTAATGGCG TGGGGGCGTT AGGATTAGAG CCGATTTTAA AGGCTTTAAA CATTGATTTT      300
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SEQ ID NO:149:

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/487,032*

INPUT SET: S8924.raw

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8075
8076    AGCAGCCTTT ATAGCGATCC TGATGGGGAT TTTCCTAACC ACCACCCAGA CCCTAGCGAA    360
8077
8078    GCGAAAAACT TAAAAGACTT AGAAAAACAC ATGCGAGAAA ACGCTATTTT AATAGGCTTT    420
8079
8080    GCTTTTGATG GCGATGCGGA TAGGATTGCG ATGCTAAGCT CTCATCATAT CTATGCGGGC    480
8081
8082    GATGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC AAGGCATCAC CCCTTTTGTG    540
8083
8084    ATCGGCGAAG TCAAATGCTC TCAAGTGATG TATAACGCAA TCAATACTTT TGGTAAGACG    600
8085
8086    CTCATGTATA AAACCGGGCA TAGCAATTTA AAAATCAAGC TCAAAGAAAC TAATGCGCAT    660
8087
8088    TTTGCGGCTG AAATGAGCGG GCATATCTTT TTTAAAGAAC GCTATTTTGG CTATGATGAC    720
8089
8090    GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG AACAAAGTCC AAGCGACTTG    780
8091
8092    GAAAACACCA TTAAAAACCT CCCCTATTCC TACACCACGC CTGAAGAAAA AATCGCCGTG    840
8093
8094    AGCGAAGAAG AAAAATTTGA AATCATTCGC AACTTACAAG AAGCGCTTAA AAACCCGCCA    900
8095
8096    AGCCATTTCC CTACAATCAA AGAAATCATC AGCATTGATG GCGTGAGAGT GGTTTTTGAA    960
8097
8098    CATGGCTTTG GGCTTATTCG CGCAAGCAAC ACCCACCCCC TATTTAGTCA GCCGCTT     1017
8099
8100
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8615    (2) INFORMATION FOR SEQ ID NO:162:
8616
8617        (i) SEQUENCE CHARACTERISTICS:
8618            (A) LENGTH: 753 base pairs
8619    E:
8620            (A) ORGANISM: Helicobacter pylori
8621
8622        (ix) FEATURE:
8623            (A) NAME/KEY: misc_feature
8624            (B) LOCATION: 1...300
8625            (D) OTHER INFORMATION: /note= " UDP-N-ACETYLMURAMYL-TRIPEPTIDE
8626    SYNTHETASE"
8627
8628        (xi) SEQUENCE DESCRIPTION:SEQ ID NO:214:
8629
8630    ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA    60
8631
8632    AGCGAAAACG AAGAAGACAT CATTAAGGAT ATTTTAAAAG GCATCAATAA TTCTTCTAAA    120
8633
8634    GTCATTGTAG AAAAAGACCG AAAAAAGGCC ATTTTAAACG CTTTAGAAAA TTTAAAAGAC    180
8635
8636    GATGAGGTGT TGTTGATTTT AGGCAAGGGC GATGAAAACA TTCAAATCTT TAAAGACAAA    240
8637
8638    ACGATTTTTT TTAGCGACCA GGAAGTCGTT AAAGATTATT ATCTCAATTT AAAACAAGGA    300
8639
8640
```

○

```
-->   8641    (2) INFORMATION FOR SEQ ID NO:215:
      8642
      8643          (i) SEQUENCE CHARACTERISTICS:
      8644              (A) LENGTH: 240 base pairs
      8645              (B) TYPE: nucleic acid
      8646              (C) STRANDEDNESS: double
      8647              (D) TOPOLOGY: circular
      8648
      8649         (ii) MOLECULE TYPE: DNA (genomic)
      8650
      8651        (iii) HYPOTHETICAL: NO
      8652
      8653         (iv) ANTI-SENSE: NO
      8654
      8655         (vi) ORIGINAL SOURCE:
      8656              (A) ORGANISM: Helicobacter pylori
      8657
      8658         (ix) FEATURE:
      8659              (A) NAME/KEY: misc_feature
      8660              (B) LOCATION: 1...240
      8661              (D) OTHER INFORMATION: /note= "FLAGELLAR MOTOR SWITCH PROTEIN F"
      8662
      8663         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
      8664
      8665    GTGATGGACA AACTCACTAA AAGCTTGCAA ACGCAAAAAA ACTTCGCTTA TTTAGGCAAA          60
      8666
      8667    ATCAAGCCCC AACAACTCGC TGATTTCATC ATTAACGAAC ACCCTCAAAC CATCGCCTTG         120
      8668
      8669    ATTTTGGCCC ACATGGAARC CCCTAATGCG GCTGAAACTT TGAGCTATTT CCCTGATGAA         180
      8670
      8671    ATGAAAGCCG AGATTTCCAT TAGAATGGCG AATTTTAGGC GAAATATCGC CCCAAGTGGT         240
      8672
      8673
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```
      8973    (2) INFORMATION FOR SEQ ID NO:224:
      8974
      8975          (i) SEQUENCE CHARACTERISTICS:
      8976              (A) LENGTH: 1263 base pairs
      8977              (B) TYPE: nucleic acid
      8978              (C) STRANDEDNESS: double
      8979              (D) TOPOLOGY: circular
      8980
      8981         (ii) MOLECULE TYPE: DNA (genomic)
      8982
      8983        (iii) HYPOTHETICAL: NO
      8984
      8985         (iv) ANTI-SENSE: NO
      8986
      8987         (vi) ORIGINAL SOURCE:
      8988              (A) ORGANISM: Helicobacter pylori
      8989
-->   8990         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:SEQ ID NO:224:
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INPUT SET: S8924.raw

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8994    TTTGCAGAGG GGGAAACTCC TTTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC    120
8995
8996    ACTATCATAG GCAAAATGGT AGATAGTATC AAAAGATACG AAGAGATTAT TTCTAAGGCT    180
8997
8998    CAAGCTCAAG TCAATCAGTT ACAAAAAGTC AATAACATGA TAAATACGAC TAATTCTTTG    240
8999
9000    ATTAGTAGTA GTGCTATCAC TTTAGCCAAT CCTATGCAAG TTTTACAAAA CGCTCAGTAT    300
9001
9002    CAAATAGAGA GCATTAGATA CAACTATGAG AATTTAAAGC AAAGCATAGA AAATTGGAAC    360
9003
9004    GCACAAAATT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTTGGCT TAATGTCAAT    420
9005
9006    GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAAT    480
9007
9008    GGCGAACAAA CCCAAACCGC AAGAGATGTG CAAAATCTCA TTCAGTCCAT TAGTGGCAGT    540
9009
9010    GGCTATGGAA ACATGCAATC ACTTGCTGGG GAATTGAGTG GTAGAGCGTG GGGGGAAATG    600
9011
9012    TTGTGTAAAA TGGTAAACGA TAGTAATTAT GAAAGCGAGC AAGCTCTTTT AGCAACAGGC    660
9013
9014    AATAACCCAG AAGAGCAAAA ACGAAGATTT TTGCTTAGAG TAAAGAAAAA GGTTAATGAT    720
9015
9016    AATAAGCAGT TAAAAGATAA ACTTGACCCA TTTCTAAAAA GACTTGATGT CCTACAAACT    780
9017
9018    GAGTTTGGTG TAACTGACCC TACAGCTAAC CATAATAAGC AAGGGATACA TTATTGCACA    840
9019
9020    GAAAATAAAG AGACAGGTAA ATGCGACCCT ATTAAAAATG TATTTAGGAC AACTCGCTTA    900
9021
9022    GATAACGAAT TAGAACAAGA AATCCAAACG CTCACACTTG ATTTAATCAA AGCCTCCAAT    960
9023
9024    AAAGACGCTC AAAGCCAAGC CTACGCAAAT TTCAATCAAA GGATTAAATT ACTTACTCTA    1020
9025
9026    AAATATTTAA AAGAAATTAC CAATCAAATG CTCTTTTTAA ATCAAACAAT GGCAATGCAA    1080
9027
9028    AGCGAGATTA TGACAGATGA TTATTTTAGG CAAAATAATG ATGGCTTTGG GGAAAAAGAA    1140
9029
9030    AACCATATAG ACGAACAATT AACGCAAAAA AGAATAAACG AAAGAGAAAG AGCTAGAATA    1200
9031
9032    TACTTTCAAA ACCCTAATGT TAAATTTGAC CAATTTGGCT TTCCCATTTT TAGTATATGG    1260
9033
9034    GAT                                                                 1263
9035
9036
```

```
9101    (2) INFORMATION FOR SEQ ID NO:227:
9102
9103        (i) SEQUENCE CHARACTERISTICS:
9104            (A) LENGTH: 2$bL      À
9105    %% A8   D   D   A     â !  "(        A      B   ð (   F
-->  9106    ! P   !P   +h B0   8  â
```

(handwritten note:) disk couldn't be read after this point,

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/487,032*

INPUT SET: S8924.raw

--> 9107 4 Ð 0,!$ D (Q! ("

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Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer
program, called Checker, that will aid applicants in identifying
and correcting errors prior to making submissions for compliance
with the Requirements for Patent Applications Containing
Nucleotide Sequence and/or Amino Acid Sequence Disclosures
(sequence rules: 37 CFR 1.821 through 1.825). (Final rules were
published in the *Federal Register* (55 FR 18230) on May 1, 1990,
and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on
May 15, 1990.)

Checker is a DOS-based software program that is intended to
assist users in determining whether errors may be present in the
sequence listings, and is not intended to guarantee that the
submission is error-free.

The most current version of the software will be available via
computer downloading (details below). Copies on diskette are
also available. Updated software versions will not be
automatically mailed out; any updates will be announced in the
PTO *Official Gazette.*

The software can be accessed/requested in the following
locations:
1)   Dial-up access to the Patent and Trademark Office Bulletin
     Board System.
     Phone number: 703-305-8950
     Cost: Free-of-charge
2)   Dial-up access through the Internet. FTP site: ftp.uspto.gov
     Login as "anonymous". Software is in directory /pub/checker
     Cost: Free-of-charge
3)   For diskette copies, telephone requests to 703-308-0322.
     Cost: $25.00

For Further Information Contact: Meredith Beckhardt at 703-308-4212.

CRF Diskette Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following CRF diskette:

Application Serial Number: **08/487,032**

Filing Date: **6/7/95**

Classification: _____

Date Reviewed by STIC: **2/23/96**

Point-of-Contact / Telephone No: __**Meredith Beckhardt**__
__**703-308-4212**__

Nature of Problem:

☑ The CRF diskette was:
- ☐ Damaged
- ☑ Unreadable — *see attached. Only parts of*
- ☐ Blank (no files present on the floppy disk) *the file could be read.* ⟶

☐ A computer virus was detected on the diskette. The STIC will not process the diskette through the Data Capture System.

Name of the virus: _____

☐ The CRF diskette contains an error that disrupts normal processing, as explained below:

- ☐ The Sequence Listing was not converted into ASCII (DOS) text
- ☐ See attached pages for clarification --->
- ☐ Other: _____

_____
_____
_____
_____
_____

9/7/95